

PATENT APPLICATION File No.: 98-10D1

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Wen-feng Xu, Scott R. Presnell, David P.

Yee, Donald C. Foster

Serial No.: 09/371,333 Group Art Unit: 1646

Filed: August 10, 1999 Examiner: John D. Ulm

For: PROTEASE-ACTIVATED RECEPTOR PAR4 (ZCHEMR2)

LETTER REGARDING SUBSTITUTE SEQUENCE LISTING

Commissioner for Patents Washington, DC 20231

Sir:

Submitted herewith is a substitute copy of the sequence listing. The substitute sequence listing contains no new matter and is now compliant with the revised sequence rules under 37 C.F.R. § 1.821-1.825.

Also submitted herewith is a sequence listing diskette for the above-captioned application. The content of substitute sequence listing and the enclosed sequence listing diskette is the same and, where applicable, includes no new matter as required by 37 CFR 1.821-1.825.

Respectfully submitted,

Phillip B.C. Jones, J.D., Ph.D.

Registration No. 38,195



1

SEQUENCE LISTING

<110> Xu, Wenfeng
 Presnell, Scott R.
 Yee, David P.
 Foster, Donald C.

<120> PROTEASE-ACTIVATED RECEPTOR PAR4
 (ZCHEMR2)

<130> 98-10D1

<140> US 09/371,333

<141> 1999-08-10

<150> US 09/053,866

<151> 1998-04-01

<160> 21

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<213> Homo sapiens

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<221> CDS

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ggtccggcga ggcaggaagc ctgaggccac agcccagagc agcctgagtg cagtc atg 178

Met

1

05

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Trp Gly Arg Leu Leu Leu Trp Pro Leu Val Leu Gly Phe Ser Leu Ser 5 10 15

ggc ggc acc cag acc ccc agc gtc tac gac gag agc ggg agc acc gga 274

Gly Gly Thr Gln Thr Pro Ser Val Tyr Asp Glu Ser Gly Ser Thr Gly 20 25 30

ggt ggt gat gac agc acg ccc tca atc ctg cct gcc ccc cgc ggc tac 322

Gly Gly Asp Asp Ser Thr Pro Ser Ile Leu Pro Ala Pro Arg Gly Tyr 35 40 45

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Pro Gly Gln Val Cys Ala Asn Asp Ser Asp Thr Leu Glu Leu Pro Asp 50 55 60 65

age tea egg gea etg ett etg gge tgg gtg eec ace agg etg gtg eec 418

Ser Ser Arg Ala Leu Leu Leu Gly Trp Val Pro Thr Arg Leu Val Pro
70 75 80

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Ala Leu Tyr Gly Leu Val Leu Val Gly Leu Pro Ala Asn Gly Leu 85 90 95

gcg ctg tgg gtg ctg gcc acg cag gca cct cgg ctg ccc tcc acc atg 514

Ala Leu Trp Val Leu Ala Thr Gln Ala Pro Arg Leu Pro Ser Thr Met
100 105 110

ctg ctg atg aac ctc gcg act gct gac ctc ctg ctg gcc ctg gcg ctg 562

Leu Leu Met Asn Leu Ala Thr Ala Asp Leu Leu Leu Ala Leu 115 120 125

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Glu	Ala	Ala	Cys	Arg 150	Leu	Ala	Thr	Ala	Ala 155	Leu	Tyr	Gly	His	Met 160	Tyr
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Gly	Ser	Val	Leu 165	Leu	Leu	Ala	Ala	Val 170	Ser	Leu	Asp	Arg	Tyr 175	Leu	A1 a
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Leu	Val	His 180	Pro	Leu	Arg	Ala	Arg 185	Ala	Leu	Arg	Gly	Arg 190	Arg	Leu	Ala
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Leu	Gly 195	Leu	Cys	Met	Ala	A1a 200	Trp	Leu	Met	Ala	Ala 205	Ala	Leu	Ala	Leu
ссс 850	ctg	aca	ctg	cag	cgg	cag	acc	ttc	cgg	ctg	gcg	cgc	tcc	gat	cgc
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Val	Leu	Cys	His	Asp 230	Ala	Leu	Pro	Leu	Asp 235	Ala	Gln	Ala	Ser	His 240	Trp
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cat tac tcg gac ccg agc ccc agc gcc tgg ggc aac ctc tat ggt gcc 1138

His Tyr Ser Asp Pro Ser Pro Ser Ala Trp Gly Asn Leu Tyr Gly Ala 310 315 320

tac gtg ccc agc ctg gcg ctg agc acc ctc aac agc tgc gtg gat ccc 1186

Tyr Val Pro Ser Leu Ala Leu Ser Thr Leu Asn Ser Cys Val Asp Pro 325 330 335

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Phe Ile Tyr Tyr Val Ser Ala Glu Phe Arg Asp Lys Val Arg Ala 340 345 350

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Ala Glu Gly Gly Ser Arg Gly Met Gly Thr His Ser Ser Leu Leu Gln 370 380 385

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cttcctggga cctcagaatg tgaccttatt tggaaatagg gttgttacaa ctgtcactag 1450

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4690
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4750
ccccagcccc tggcaaccac aaatctttcc aactctacgg atttgcctgt tctgggcatt
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                               25
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Asp 65	Ser	Ser	Arg	Ala	Leu 70	Leu	Leu	Gly	Trp	Va1 75	Pro	Thr	Arg	Leu	Val 80
			-	85					90					Asn 95	
			100					105					110	Ser	
		115					120					125		Leu	
	130					135					140		·	Pro	
145					150					155		_	_	His	160
				165					170			·		Tyr 175	
			180					185					190	Arg	
		195		·			200	•				205		Leu	
	210					215					220			Ser	
225					230					235				Ser	240
				245					250					Leu 255 Leu	
			260					265					270	Val	
		275					280					285		Leu	
	290					295					300			Tyr	
305				·	310					315				Val	320
				325					330					335 Val	
			340	_	_			345			_	•	350	Lys	•
ATU	ury	355	1110	uIII	лу	JCI	360	ury	ush	1111	vui	365	JUI	Lys	711 u

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                                             380
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 Gln
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       <221> variation
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       <223> N is any nucleotide.
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ytngarytnc engaywsnws nmgngenytn ytnytnggnt gggtneenae nmgnytngtn
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 congonytht ayggnythgt nythgtngth ggnythcong chaayggnyt ngonythtgg
300
 gtnytngcna cncargenec nmgnytnech wsnachatgy tnytnatgaa yytngchach
360
 gengayytny tnytngenyt ngenytneen cenmgnathg entayeayyt nmgnggnear
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 tayggnwsng tnytnytnyt ngcngcngtn wsnytngaym gntayytngc nytngtncay
540
 conythmana chmanachyt hmanaghman manythachy thaganythta yatagchach
 tggytnatgg engengenyt ngenytneen ytnaenytne armgnearae nttymgnytn
660
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ytnytnytny tnytncayta ywsngayccn wsnccnwsng cntggggnaa yytntayggn
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taytaygtnw sngcngartt ymgngayaar gtnmgngcng gnytnttyca rmgnwsnccn
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                  5
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                 5
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                                                         15
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 1
                 5
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                 5
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Asp Thr Leu Glu Leu Pro Asp Ser Ser
            20
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CS Cont